SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT: WALLACH, David
                  BOLDIN, Mark
                  VARFOLOMEEV, Eugene
                  METT, Igor

  (ii) TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/APO1
                      RECEPTORS

 (iii) NUMBER OF SEQUENCES: 2

  (iv) CORRESPONDENCE ADDRESS:
      (A) ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
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      (C) CITY: Washington
      (D) STATE: D.C.
      (E) COUNTRY: United States of America
      (F) ZIP: 20004

   (v) COMPUTER READABLE FORM:
      (A) MEDIUM TYPE: Floppy disk
      (B) COMPUTER: IBM PC compatible
      (C) OPERATING SYSTEM: PC-DOS/MS-DOS
      (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

  (vi) CURRENT APPLICATION DATA:
      (A) APPLICATION NUMBER: 08/860,082
      (B) FILING DATE: 19-AUG-1997

 (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: PCT/US95/16542
      (B) FILING DATE: 14-DEC-1995

 (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: IL 112022
      (B) FILING DATE: 15-DEC-1994

 (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: IL 112692
      (B) FILING DATE: 19-FEB-1995

 (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: IL 114615
      (B) FILING DATE: 16-JUL-1995

(viii) ATTORNEY/AGENT INFORMATION:
      (A) NAME: BROWDY, Roger L.
      (B) REGISTRATION NUMBER: 25,618
      (C) REFERENCE/DOCKET NUMBER: WALLACH=16

  (ix) TELECOMMUNICATION INFORMATION:
      (A) TELEPHONE: (202) 628-5197
      (B) TELEFAX: (202) 737-3528

(2) INFORMATION FOR SEQ ID NO:1:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1701 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
    (A) NAME/KEY: CDS
    (B) LOCATION: 1..768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GTG AAT CAG GCA CCG GAG TGC AGG TTC GGG GGT GGA ATC CTT GGG CCG        48
Val Asn Gln Ala Pro Glu Cys Arg Phe Gly Gly Gly Ile Leu Gly Pro
 1               5                   10                  15

CTG GGC AAG CGG CGA GAC CTG GCC AGG GCC AGC GAG CCG AGG ACA GAG        96
Leu Gly Lys Arg Arg Asp Leu Ala Arg Ala Ser Glu Pro Arg Thr Glu
                20                  25                  30

GGC GCG CGG AGG GCC GGG CCG CAG CCC CGG CCG CTT GCA GAC CCC GCC       144
Gly Ala Arg Arg Ala Gly Pro Gln Pro Arg Pro Leu Ala Asp Pro Ala
            35                  40                  45

ATG GAC CCG TTC CTG GTG CTG CTG CAC TCG GTG TCG TCC AGC CTG TCG       192
Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
     50                  55                  60

AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG CGC GTG GTC       240
Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Val
 65                  70                  75                  80

AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC TTC TCC ATG       288
Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
                85                  90                  95

CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG CTC CTG CGC       336
Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
                100                 105                 110

GAG CTG CTC GCC TCC CTG CGG CGC CAC GAC CTG CTG CGG CGC GTC GAC       384
Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
            115                 120                 125

GAC TTC GAG GCG GGG GCG GCG GCC GGG GCC GCG CCT GGG GAA GAA GAC       432
Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
     130                 135                 140

CTG TGT GCA GCA TTT AAC GTC ATA TGT GAT AAT GTG GGG AAA GAT TGG       480
Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
145                 150                 155                 160

AGA AGG CTG GCT CGT CAG CTC AAA GTC TCA GAC ACC AAG ATC GAC AGC       528
Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
                165                 170                 175

ATC GAG GAC AGA TAC CCC CGC AAC CTG ACA GAG CGT GTG CGG GAG TCA       576
Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
                180                 185                 190

CTG AGA ATC TGG AAG AAC ACA GAG AAG GAG AAC GCA ACA GTG GCC CAC       624
Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
                195                 200                 205

CTG GTG GGG GCT CTC AGG TCC TGC CAG ATG AAC CTG GTG GCT GAC CTG       672
Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
            210                 215                 220

GTA CAA GAG GTT CAG CAG GCC CGT GAC CTC CAG AAC AGG AGT GGG GCC       720
Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
225                 230                 235                 240
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ATG TCC CCG ATG TCA TGG AAC TCA GAC GCA TCT ACC TCC GAA GCG TCC   768
Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser
                245   250   255

TGATGGGCCG CTGCTTTGCG CTGGTGGACC ACAGGCATCT ACACAGCCTG GACTTTGGTT   828

CTCTCCAGGA AGGTAGCCCA GCACTGTGAA GACCCAGCAG GAAGCCAGGC TGAGTGAGCC   888

ACAGACCACC TGCTTCTGAA CTCAAGCTGC GTTTATTAAT GCCTCTCCCG CACCAGGCCG   948

GGCTTGGGCC CTGCACAGAT ATTTCCATTT CTTCCTCACT ATGACACTGA GCAAGATCTT   1008

GTCTCCACTA AATGAGCTCC TGCGGGAGTA GTTGGAAAGT TGGAACCGTG TCCAGCACAG   1068

AAGGAATCTG TGCAGATGAG CAGTCACACT GTTACTCCAC AGCGGAGGAG ACCAGCTCAG   1128

AGGCCCAGGA ATCGGAGCGA AGCAGAGAGG TGGAGAACTG GGATTTGAAC CCCCGCCATC   1188

CTTCACCAGA GCCCATGCTC AACCACTGTG GCGTTCTGCT GCCCCTGCAG TTGGCAGAAA   1248

GGATGTTTTT GTCCCATTTC CTTGGAGGCC ACCGGGACAG ACCTGGACAC TAGGGTCAGG   1308

CGGGGTGCTG TGGTGGGGAG AGGCATGGCT GGGGTGGGGG TGGGGAGACC TGGTTGGCCG   1368

TGGTCCAGCT CTTGGCCCCT GTGTGAGTTG AGTCTCCTCT CTGAGACTGC TAAGTAGGGG   1428

CAGTGATGGT TGCCAGGACG AATTGAGATA ATATCTGTGA GGTGCTGATG AGTGATTGAC   1488

ACACAGCACT CTCTAAATCT TCCTTGTGAG GATTATGGGT CCTGCAATTC TACAGTTTCT   1548

TACTGTTTTG TATCAAAATC ACTATCTTTC TGATAACAGA ATTGCCAAGG CAGCGGGATC   1608

TCGTATCTTT AAAAAGCAGT CCTCTTATTC CTAAGGTAAT CCTATTAAAA CACAGCTTTA   1668

CAACTTCCAT ATTACAAAAA AAAAAAAAAA AAA   1701

(2) INFORMATION FOR SEQ ID NO:2:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 256 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Asn Gln Ala Pro Glu Cys Arg Phe Gly Gly Gly Ile Leu Gly Pro
 1   5   10   15

Leu Gly Lys Arg Arg Asp Leu Ala Arg Ala Ser Glu Pro Arg Thr Glu
            20   25   30

Gly Ala Arg Arg Ala Gly Pro Gln Pro Arg Pro Leu Ala Asp Pro Ala
            35   40   45

Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
        50   55   60

Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Val
65   70   75   80

Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
                85   90   95

50

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Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
            100                 105                 110

Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
            115                 120                 125

Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
    130                 135                 140

Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
145                 150                 155                 160

Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
            165                 170                 175

Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
            180                 185                 190

Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
        195                 200                 205

Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
    210                 215                 220

Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
225                 230                 235                 240

Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser
                245                 250                 255
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